Appendix III

Alignment of SEQ ID NO: 1479 of Tang et al with the sequence of GenBank Accession No. BAA23691.2

Score = 1827 bits (4732), Expect = 0.0, Method: Compositional matrix adjust. Identities = 877/879 (99%), Positives = 878/879 (99%), Gaps = 0/879 (0%) Query SCKYCDFRSHDMTQFVGHMNSEHTDFNKDPTFVCSGCSFLAKTPEGLSLHNATCHSGEAS ${\tt SCKYCDFRSHDMTQFVGHMNSEHTDFNKDFTFVCSGCSFLAKTFEGLSLHNATCHSGEAS}$ SCKYCDFRSHDMTQFVGHMNSEHTDFNKDFTFVCSGCSFLAKTFEGLSLHMATCHSGEAS Sbjet 1 FYWNVAKPDNHYYYEQSIPESTSTPDLAGEPSAEGADGQAEIIITKTPIMKIMKGKARAK Query 138 FVWNVAKPDNHVVVEOSIPESTSTPDLAGEPSAEGADGOAEIIITKTPIMKIMKGKAEAK Sbjet 61 fywnyakpdnhyyyegsipeststpdlagepsaegadgQaeiiitktpimkimkgkaeak 120 Query 198 KIHTLKENVPSQPVGEALPKLSTGEMEVREGDHSFINGAVPVSQASASSAKNPHAANGPL 257 KIHTLKENYPSQPYGEALPKLSTGEMEYREGDHSFINGAYPYSQASASSAKNPHAANGPL Sbjct 121 KIHTLKENVPSQPVGEALPKLSTGEMEVREGDHSFINGAVPVSQASASSAKNPHAANGPL 180 258 IGTYPVLPAGIAQFLSLQQQPPVHAQHHYHQPLPTAKALPKYMIPLSSIPTTSAAMDSNS Query 317igtvpvlpagiaqflslqqqppvhaqhhvhqplptakalfkvmiplssifti+aamdsns Sbjet 181 IGTVFVLPAGIAQFLSLQQQPFVHAQHHVHQFLPTAKALPKVMIPLSSIPTYNAAMDSNS 240 318 FLKNSFHKFPYPTKAELCYLTVVTKYPEEOLKIWFTAORLKOGISWSPEEIEDARKKMFW Ouerv flknsfhkfpyptkaelcyltvytkypeeqlkiwftaqrlkqgiswspeeiedarkkmfn Sbjct 241 FLKNSFHKFPYPTKAELCYLTVVTKYPEEQLKIWFTAQRLKQGISWSPEEIEDARKKMFN 300 TVIQSVPQFTITVLNTPLVASAGNVQHLIQAALPGHVVGQPEGTGGGLLVTQPLMANGLQ Query 378 TVIQSVPQPTITVLNTPLVASAGNVQHLIQAALPGHVVGQPEGTGGGLLVTQPLMANGLQ Sbjet 301 TVIQSVPQPTITVLNTPLVASAGNVQHLIQAALPGHVVGQPEGTGGGLLVTQPLMANGLQ 360 Query 438 ATSSPLPLTVTSVPKQPGVAPINTVCSNTTSAVKVVNAAQSLLTACPSITSQAFLDASIY 497 ATSSPLPLTVTSVPKOPGVAPINTVCSNTTSAVKVVNAAOSLLTACPSITSOAFLDASIY Sbjet 351 ATSSPLPLTYTSVPKQPGVAPINTVCSNTTSAVKVVNAAQSLLTACPSITSQAFLDASIY 420 KNKKSHEQLSALKGSFCRNQFPGQSEVEHLTKYTGLSTREVRKWFSDRRYHCRNLKGSRA Query 498 KNKKSHEQLSALKGSFCRNQFPGQSEVEHLTKVTGLSTREVRKWFSDRRYHCRNLKGSRA 421 KNKKSHEQLSALKGSFCRNQFPGQSEVEHLTKVTGLSTREVRKWFSDRRYHCRNLKGSRA 480 Sbjot 558 MIPGDRSSIIIDSVPEVSFSPSSKVPEVTCIPTTATLATHPSAKRQSWEQTPDFTPTKYK 617 Querv MIPGDHSSIIIDSVPEVSFSPSSKVPEVTCIPTTATLATHPSAKRQSMHQTPDFTPTKYK Sbjot 481 MIPGDHSSIIIDSVPEVSESPSSKVPEVTCIPTTATLATHPSAKRQSWHQTPDFTPTKYK 540 Query 618 EFAPEQLRALESSFAQNFLPLDEELDRLFSETKMTRREIDSWFSERRKEVNAHETEKABE ERAPEQLRALESSFAQNFLPLDEELDRLRSETKMTRREIDSWFSERRKKVNAEETKKAEE Sbjet 541 ERAPEQLRALESSFAQNPLPLDEELDPLRSETKMTRREIDSWFSERRKKVNAEETKKAEE 600 Query 678 MASQEEEEAAEDEGGEEDLASELRVSGENGSLEMPSSHILAERKVSPIKINLKNLRVTEA 737 MASQEEREAAEDEGGEEDLASELRVSGENGSLEMPSSHILAERKVSPIKINLKNLRVTEA Sbjet 601 NASQEEEEAAEDEGGEEDLASELRVSGENGSLEMPSSHILAERKVSPIKINLKNLRVTEA 660 738 ngrneipglgacdfeddesnklaeolpgkvsckktaoorhllrolfvotompsnodidsi 797 Query NGRNE IPGLGACDPEDDESNKLABQLPGKVSCKKTAQQRHLLRQLFVQTQMPSNQDYDS I 661 NGRNEIPGLGACDPEDDESNKLAEQLPGKVSCKKTAQQRHLLRQLFVQTQWPSNQDYDSI 720 Sbjet 798 MAQTGLPRPEVVRWFGDSRYALKNGQLKWYEDYKRGNFPPGLLVIAPGNRELLQDYYMTH 857 Query MAQTGLPRPEYYRWFGDSRYALKNGQLKWYEDYKRGNFPPGLLY IAPGNRELLQDYYMTH Sbjet 721 MAQTGLPRPEVVRMPGDSRYALKNGQLKWYEDYKRGNPPPGLLVIAPGNRELLQDYYMTH 780 Query KMLYEEDLQNLCDKTQMSSQQVKQWFAEKMGEETRAVADTGSEDQGPGTGELTAVHKGMG 917 KMLYEEDLQNLCDKTQMSSQQVKQWFAEKMGEETRAVADTGSEDQGFGT ELTAVHKGMG 781 KMLYBEDLQMLCDKTQMSSQQVKQWFAEKMGBETPAVADTGSEDQGFGTTELTAVHKGMG Sbjet 918 DTYSEVSENSESWEPRVPEASSEPFDTSSPQAGRQLETD Query DTYSEVSENSESWEPRVPEASSEPFDTSSPQAGRQLETD Sbjet 841 DTYSEVSENSESWEFRVPEASSEPFDTSSPQAGRQLETD 879